

FIGURE 1A

Input file Fbh56919FL2.seq
Sequence length 3003

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TTCGGCACCAGGCTGCTGCGGGGGGACTCTTTCTGAGGTTACTGTGGAGCACCCAAAGTCTGTCAGCCTCTGGCCGTGC
AAACAGGCACCCAGAGGAACCAGACCTTGCTTATTACCCACAGCCTGGGACTGTCTTCTCCAGAGTCTCCATCAGCTT
TGCTAATCGACTGATTGGAATAATTCTCTCAAACACCACCAAGTCAAGGATACAGGCAGCAGCGGCTCCCCCTGTTGTAT
GGACATTCTGCACCCGAAACTGATAGCTGAGTCTGAAGTTTTATGTTATGAAACAGAAGAACTTTTCATCCCAGCACAT

      M   D   E   S   A   L   T   L   G   T   I   D   V
GATTTGGGAATTACACTTTGTGAC ATG GAT GAA TCT GCA CTG ACC CTT GGT ACA ATA GAT GTT      13
                                           39

S   Y   L   P   H   S   S   E   Y   S   V   G   R   C   K   H   T   S   E   E      33
TCT TAT CTG CCA CAT TCA TCA GAA TAC AGT GTT GGT CGA TGT AAG CAC ACA AGT GAG GAA      99

W   G   E   C   G   F   R   P   T   V   F   R   S   A   T   L   K   W   K   E      53
TGG GGT GAG TGT GGC TTT AGA CCC ACC GTC TTC AGA TCT GCA ACT TTA AAA TGG AAA GAA      159

S   L   M   S   R   K   R   P   F   V   G   R   C   C   Y   S   C   T   P   Q      73
AGC CTA ATG AGT CGG AAA AGG CCA TTT GTT GGA AGA TGT TGT TAC TCC TGC ACT CCC CAG      219

S   W   D   K   F   F   N   P   S   I   P   S   L   G   L   R   N   V   I   Y      93
AGC TGG GAC AAA TTT TTC AAC CCC AGT ATC CCG TCT TTG GGT TTG CGG AAT GTT ATT TAT      279

I   N   E   T   H   T   R   H   R   G   W   L   A   R   R   L   S   Y   V   L      113
ATC AAT GAA ACT CAC ACA AGA CAC CGC GGA TGG CTT GCA AGA CGC CTT TCT TAC GTT CTT      339

F   I   Q   E   R   D   V   H   K   G   M   F   A   T   N   V   T   E   N   V      133
TTT ATT CAA GAG CGA GAT GTG CAT AAG GGC ATG TTT GCC ACC AAT GTG ACT GAA AAT GTG      399

L   N   S   S   R   V   Q   E   A   I   A   E   V   A   A   E   L   N   P   D      153
CTG AAC AGC AGT AGA GTA CAA GAG GCA ATT GCA GAA GTG GCT GCT GAA TTA AAC CCT GAT      459

G   S   A   Q   Q   Q   S   K   A   V   N   K   V   K   K   K   A   K   R   I      173
GGT TCT GCC CAG CAG CAA TCA AAA GCC GTT AAC AAA GTG AAA AAG AAA GCT AAA AGG ATT      519

L   Q   E   M   V   A   T   V   S   P   A   M   I   R   L   T   G   W   V   L      193
CTT CAA GAA ATG GTT GCC ACT GTC TCA CCG GCA ATG ATC AGA CTG ACT GGG TGG GTG CTG      579

L   K   L   F   N   S   F   F   W   N   I   Q   I   H   K   G   Q   L   E   M      213
CTA AAA CTG TTC AAC AGC TTC TTT TGG AAC ATT CAA ATT CAC AAA GGT CAA CTT GAG ATG      639

V   K   A   A   T   E   T   N   L   P   L   L   F   L   P   V   H   R   S   H      233
GTT AAA GCT GCA ACT GAG ACG AAT TTG CCG CTT CTG TTT CTA CCA GTT CAT AGA TCC CAT      699

I   D   Y   L   L   L   T   F   I   L   F   C   H   N   I   K   A   P   Y   I      253
ATT GAC TAT CTG CTG CTC ACT TTC ATT CTC TTC TGC CAT AAC ATC AAA GCA CCA TAC ATT      759

A   S   G   N   N   L   N   I   P   I   F   S   T   L   I   H   K   L   G   G      273
GCT TCA GGC AAT AAT CTC AAC ATC CCA ATC TTC AGT ACC TTG ATC CAT AAG CTT GGG GGC      819

F   F   I   R   R   R   L   D   E   T   P   D   G   R   K   D   V   L   Y   R      293
TTC TTC ATA CGA CGA AGG CTC GAT GAA ACA CCA GAT GGA CGG AAA GAT GTT CTC TAT AGA      879

A   L   L   H   G   H   I   V   E   L   L   R   Q   Q   Q   F   L   E   I   F      313
GCT TTG CTC CAT GGG CAT ATA GTT GAA TTA CTT CGA CAG CAG CAA TTC TTG GAG ATC TTC      939

L   E   G   T   R   S   R   S   G   K   T   S   C   A   R   A   G   L   L   S      333
CTG GAA GGC ACA CGT TCT AGG AGT GGA AAA ACC TCT TGT GCT CGG GCA GGA CTT TTG TCA      999

V   V   V   D   T   L   S   T   N   V   I   P   D   I   L   I   I   P   V   G      353
GTT GTG GTA GAT ACT CTG TCT ACC AAT GTC ATC CCA GAC ATC TTG ATA ATA CCT GTT GGA      1059

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FIGURE 1B

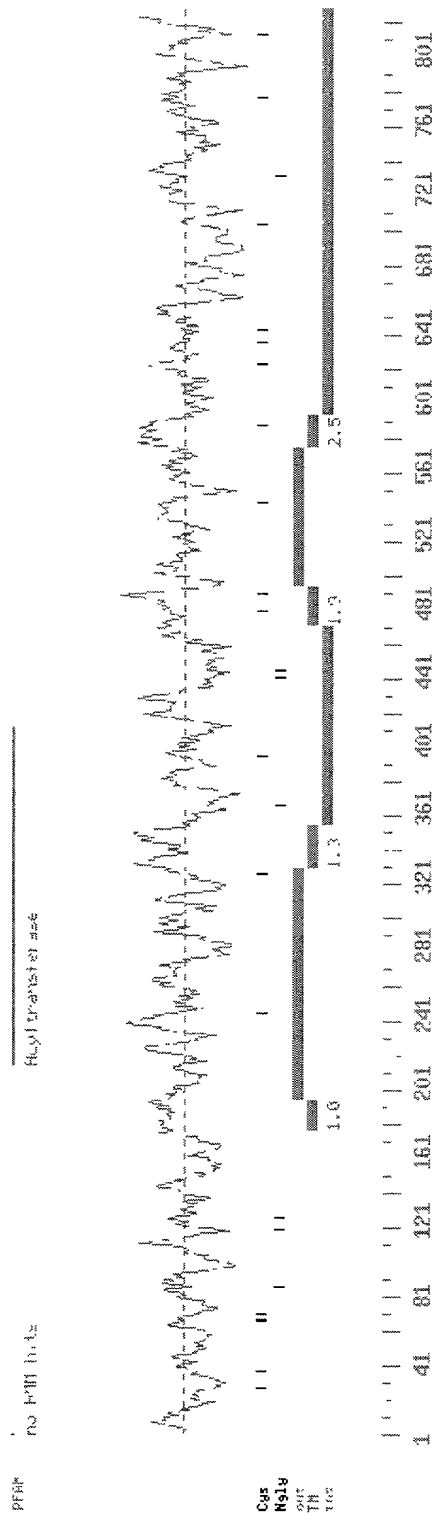
I	S	Y	D	R	I	I	E	G	H	Y	N	G	E	Q	L	G	K	P	K	373
ATC	TCC	TAT	GAT	CGC	ATT	ATC	GAA	GGT	CAC	TAC	AAT	GGT	GAA	CAA	CTG	GGC	AAA	CCT	AAG	1119
K	N	E	S	L	W	S	V	A	R	G	V	I	R	M	L	R	K	N	Y	393
AAG	AAT	GAG	AGC	CTG	TGG	AGT	GTA	GCA	AGA	GGT	GTT	ATT	AGA	ATG	TTA	CGA	AAA	AAC	TAT	1179
G	C	V	R	V	D	F	A	Q	P	F	S	L	K	E	Y	L	E	S	Q	413
GGT	TGT	GTC	CGA	GTG	GAT	TTT	GCA	CAG	CCA	TTT	TCC	TTA	AAG	GAA	TAT	TTA	GAA	AGC	CAA	1239
S	Q	K	P	V	S	A	L	L	S	L	E	Q	A	L	L	P	A	I	L	433
AGT	CAG	AAA	CCG	GTG	TCT	GCT	CTA	CTT	TCC	CTG	GAG	CAA	GCG	TTG	TTA	CCA	GCT	ATA	CTT	1299
P	S	R	P	S	D	A	A	D	E	G	R	D	T	S	I	N	E	S	R	453
CCT	TCA	AGA	CCC	AGT	GAT	GCT	GCT	GAT	GAA	GGT	AGA	GAC	ACG	TCC	ATT	AAT	GAG	TCC	AGA	1359
N	A	T	D	E	S	L	R	R	R	L	I	A	N	L	A	E	H	I	L	473
AAT	GCA	ACA	GAT	GAA	TCC	CTA	CGA	AGG	AGG	TTG	ATT	GCA	AAT	CTG	GCT	GAG	CAT	ATT	CTA	1419
F	T	A	S	K	S	C	A	I	M	S	T	H	I	V	A	C	L	L	L	493
TTC	ACT	GCT	AGC	AAG	TCC	TGT	GCC	ATT	ATG	TCC	ACA	CAC	ATT	GTG	GCT	TGC	CTG	CTC	CTC	1479
Y	R	H	R	Q	G	I	D	L	S	T	L	V	E	D	F	F	V	M	K	513
TAC	AGA	CAC	AGG	CAG	GGA	ATT	GAT	CTC	TCC	ACA	TTG	GTC	GAA	GAC	TTC	TTT	GTG	ATG	AAA	1539
E	E	V	L	A	R	D	F	D	L	G	F	S	G	N	S	E	D	V	V	533
GAG	GAA	GTC	CTG	GCT	CGT	GAT	TTT	GAC	CTG	GGG	TTC	TCA	GGA	AAT	TCA	GAA	GAT	GTA	GTA	1599
M	H	A	I	Q	L	L	G	N	C	V	T	I	T	H	T	S	R	N	D	553
ATG	CAT	GCC	ATA	CAG	CTG	CTG	GGA	AAT	TGT	GTC	ACA	ATC	ACC	CAC	ACT	AGC	AGG	AAC	GAT	1659
E	F	F	I	T	P	S	T	T	V	P	S	V	F	E	L	N	F	Y	S	573
GAG	TTT	TTT	ATC	ACC	CCC	AGC	ACA	ACT	GTC	CCA	TCA	GTC	TTC	GAA	CTC	AAC	TTC	TAC	AGC	1719
N	G	V	L	H	V	F	I	M	E	A	I	I	A	C	S	L	Y	A	V	593
AAT	GGG	GTA	CTT	CAT	GTC	TTT	ATC	ATG	GAG	GCC	ATC	ATA	GCT	TGC	AGC	CTT	TAT	GCA	GTT	1779
L	N	K	R	G	L	G	G	P	T	S	T	P	P	N	L	I	S	Q	E	613
CTG	AAC	AAG	AGG	GGA	CTG	GGG	GGT	CCC	ACT	AGC	ACC	CCA	CCT	AAC	CTG	ATC	AGC	CAG	GAG	1839
Q	L	V	R	K	A	A	S	L	C	Y	L	L	S	N	E	G	T	I	S	633
CAG	CTG	GTG	CGG	AAG	GCG	GCC	AGC	CTG	TGC	TAC	CTT	CTC	TCC	AAT	GAA	GGC	ACC	ATC	TCA	1899
L	P	C	Q	T	F	Y	Q	V	C	H	E	T	V	G	K	F	I	Q	Y	653
CTG	CCT	TGC	CAG	ACA	TTT	TAC	CAA	GTC	TGC	CAT	GAA	ACA	GTA	GGA	AAG	TTT	ATC	CAG	TAT	1959
G	I	L	T	V	A	E	H	D	D	Q	E	D	I	S	P	S	L	A	E	673
GGC	ATT	CTT	ACA	GTG	GCA	GAG	CAC	GAT	GAC	CAG	GAA	GAT	ATC	AGT	CCT	AGT	CTT	GCT	GAG	2019
Q	Q	W	D	K	K	L	P	E	P	L	S	W	R	S	D	E	E	D	E	693
CAG	CAG	TGG	GAC	AAG	AAG	CTT	CCA	GAA	CCT	TTG	TCT	TGG	AGA	AGT	GAT	GAA	GAA	GAT	GAA	2079
D	S	D	F	G	E	E	Q	R	D	C	Y	L	K	V	S	Q	S	K	E	713
GAC	AGT	GAC	TTT	GGG	GAG	GAA	CAG	CGA	GAT	TGC	TAC	CTG	AAG	GTG	AGC	CAA	TCC	AAG	GAG	2139
H	Q	Q	F	I	T	F	L	Q	R	L	L	G	P	L	L	E	A	Y	S	733
CAC	CAG	CAG	TTT	ATC	ACC	TTC	TTA	CAG	AGA	CTC	CTT	GGG	CCT	TTG	CTG	GAG	GCC	TAC	AGC	2199
S	A	A	I	F	V	H	N	F	S	G	P	V	P	E	P	E	Y	L	Q	753
TCT	GCT	GCC	ATC	TTT	GTT	CAC	AAC	TTC	AGT	GGT	CCT	GTT	CCA	GAA	CCT	GAG	TAT	CTG	CAA	2259
K	L	H	K	Y	L	I	T	R	T	E	R	N	V	A	V	Y	A	E	S	773
AAG	TTG	CAC	AAA	TAC	CTA	ATA	ACC	AGA	ACA	GAA	AGA	AAT	GTT	GCA	GTA	TAT	GCT	GAG	AGT	2319

D	I	G	V	F	K	793
G GAT	ATT	GGG	GTT	TTC	AAG	2379
T	F	L	P	Q	C	813
C ACT	TTT	CTA	CCT	CAA	TGC	2439
L	*					829
G CTG	TAG					2487

ACCAGCTTCTGGCTCAAGAGTTTGA
CAAGTGCCTTCTNCCTCCATGGATC

1000 800 600 400 200 0

Figure 2



>56919
MDESALTGTIDVSLPHSSEYVGRCKHTSEEWGECGFRFTVFRSATLKWKESLMSRKR
PFVGRCCYCTPQSWDKFFNPISLGLRNVIYINETHRHRGWLARRLSYVLFIQERDV
HKGMFATNTENVLNNSRVQEAIAEVAALNPDGSAQQQSKAVNKVKKKAKRIIQEMVAT
VSPAMIRLTGWVLLKLFNFWNQIHKQLEVMVKAATEINLPLFLPVHRSHIDYLLLT
FILFCHNIKAPYIAGNNLNIPFSTLIHKLGGFFIRRLDETPDGRKDVLYRALLHGH
VELLRQQQFLEIFLEGTRSRGKTSARAGLLSVVVDTLSTNVIPDILIPVGISYDRII
EGHYNGEQLGPKPKNESLWSVARGVIRMLRKNYGCVRVDFAPFSLKEYLESQSKPVSA
LLSLEQALLPAILPRSPDADEGRDTSINESRNATDESRRRLIANLAELHILFTASKSC
AIMSTHIVACLLLYRHRQIDLSLTVEDFFVMKEEVLARDFDLGFSGNSDEVVMHAIQLL
GNCVTITHTSRNDEFFITPSTVPSVFLNFYSNGLVHVFIMEAIIACSLYAVLNKRGLG
GPTSTPPNLSQEQLVKKAASLCYLLSNEGTSILPCQTFYQVCHETVGKFIQYGLITVAE
HDQQEDISPLAEQQWDKKLPEPLSWRSEDEDEDFGEQORDCYLVKSQSKHQQFITF
LQRLGLPLEAYSSAAIFVHNFGPVPPEYQLKLHKYLITRTERNVAVYAESATYCLVK
NAVMMFKDIGVFKETKQKRVSVLELSSTFLPQCNRQKLLLEYILSFVVL

Figure 3

Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM
 hmmpfam - search a single seq against HMM database
 HMMER 2.1.1 (Dec 1998)
 Copyright (C) 1992-1998 Washington University School of Medicine
 HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/ddm/seqanal/PFAM/pfam6.4/Pfam
 Sequence file: /prod/ddm/wspace/orfanal/oa-script.21255.seq

Query: 56919

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
-----	-----	-----	-----	----
Acyltransferase	Acyltransferase	126.1	6.4e-34	
1				

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
-----	-----	-----	-----	-----	-----	-----	-----
Acyltransferase	1/1	215	412	..	1 195 []	126.1	6.4e-34

Alignments of top-scoring domains:

Acyltransferase: domain 1 of 1, from 215 to 412: score 126.1, E = 6.4e-34

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      *->lenlpkkgpaivvsNHrSylDilvlSaalprrgpwlvrllvfiakke
      + +++++ p ++ + HrS++D+l+l ++l++++ ++ +ia ++
56919  215  KAATETNLPLFLPVHRSHIDYLLLTFILFCHN----IKAPYIASGN 257

      llkvPlIfGwlmrlagaifidRnnra....kdalaaadelvrvlellrk
      +l++P+ f++l+ ++g +fi+R+ ++++++kd l++a+ + + +ellr+
56919  258  NLNIPI-FSTLIHKLGFFIRRRLEtpdgrKDVLYRALLHGHIVELLRQ 306

      grsvliFPEGTRsrsgellppfKkGia....afrlAlkagvpivPvviv
      + + iF EGTRsrsg++ + ++G+++ + + ++ ++ i+Pv+i
56919  307  QQFLEIFLEGTRSRSGKTSC-ARAGLLsvvvdTLSTNVIPDILIIIPVGI- 354

      sgteelepneagklLrlarkkgpvtvrvlppipld..pedikelaerlr
      s++ ++e ++++ + +++kk+++++ v +++ +++++ +++++ +
56919  355  SYDRIIEGHYNGEQ--LGKPKKNESLWSVARGVIRMLrKNYGCVRVDFAQ 402

      dilvqaleel<-*
      + +++++ e+
56919  403  PFSLKEYLES 412
  
```

Figure 4A

ProDom Matches

ProDomId	Start	End	Description	Score
View Prodom PD347660	1	55	p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION MITOCHONDRIAL	250
View Prodom PD087501	51	158	p2001.1 (1) // AIP2-DLD1	77
View Prodom PD353751	56	152	p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION MITOCHONDRIAL	500
View Prodom PD037846	128	259	p2001.1 (15) PLSB(5) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE PHOSPHOLIPID GPAT BIOSYNTHESIS MITOCHONDRIAL TRANSMEMBRANE PRECURSOR MITOCHONDRION	258
View Prodom PD042466	259	590	p2001.1 (16) PLSB(4) DAPT(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE BIOSYNTHESIS PHOSPHOLIPID GPAT PRECURSOR MITOCHONDRIAL TRANSMEMBRANE MITOCHONDRION	413
View Prodom PD025192	462	649	p2001.1 (4) PLSB(3) // ACYLTRANSFERASE PHOSPHOLIPID MITOCHONDRIAL BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION	458
View Prodom PD042027	465	673	p2001.1 (6) PLSB(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE MEMBRANE PHOSPHOLIPID GPAT BIOSYNTHESIS MUTANT	80
View Prodom PD042760	650	828	p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION MITOCHONDRIAL	799

Figure 4B

View Prodom PD042760

>PD042760 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS
PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION
MITOCHONDRIAL
Length = 179

Score = 799 (286.3 bits), Expect = 1.2e-79, P = 1.2e-79
Identities = 155/179 (86%), Positives = 161/179 (89%)

Query: 650 FIQYGILTVAEHDDQEDISPSLAEQWKKLPELSWRXXXXXXXXXXXXXQDCYLKVS 709
FIQYGILTVAE DDQED+SP LAEQW+KKLPEPL+WR QDCYLKVS
Sbjct: 1 FIQYGILTVAEQDDQEDVSPGLAEQWKKLPELWNRSDEDEDSDFGEEQDCYLKVS 60

Query: 710 QSKEHQQFITFLQRLGPLEAYSSAAIFVHNFSGVPPEPYLQKLHKYLIITRERNVAV 769
Q+KEHQQFITFLQRLGPLEAYSSAAIFVHNF GPVPE EYLQKLH+YLIITRERNVAV
Sbjct: 61 QAKEHQQFITFLQRLGPLEAYSSAAIFVHNFSGVPPESEYIQLKHYLIITRERNVAV 120

Query: 770 YAESATYCLVKNVAVKMPKDIGVFKETQKRVSVLELSTTFLPQCNRQKLLEYILSFVVL 828
YAESATYCLVKNVAVKMPKDIGVFKETQKR SVLELS+TFLPQCNRQKLLEYILSFVVL
Sbjct: 121 YAESATYCLVKNVAVKMPKDIGVFKETQKRASVLELSTTFLPQCNRQKLLEYILSFVVL 179

View Prodom PD353751

>PD353751 p2001.1 (2) PLSB(2) // ACYLTRANSFERASE PHOSPHOLIPID BIOSYNTHESIS
PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT MITOCHONDRION
MITOCHONDRIAL
Length = 97

Score = 500 (181.1 bits), Expect = 2.1e-47, P = 2.1e-47
Identities = 90/97 (92%), Positives = 97/97 (100%)

Query: 56 MSKRPPFVGRCCYSCCTPQSWDKFFNPSPSLGLRNVIIYNETHTRHRCWLARRLSYVLFI 115
MSKRPPFVGRCCYSCCTPQSW++FNPSPSLGLRNVIIYNETHTRHRCWLARRLSY+LF+
Sbjct: 1 MSKRPPFVGRCCYSCCTPQSWERFNPSPSLGLRNVIIYNETHTRHRCWLARRLSYILFV 60

Query: 116 QERDVHKGMFATNVNTENVLNSSRVQEAIAEVAELNP 152
QERDVHKGMFAT++T+NVLNSSRVQEAIAEVAELNP
Sbjct: 61 QERDVHKGMFATSIDNVLNSSRVQEAIAEVAELNP 97

Figure 4C

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View Prodom PD025192

>PD025192 p2001.1 (4) PLSB(3) // ACYLTRANSFERASE PHOSPHOLIPID MITOCHONDRIAL
BIOSYNTHESIS PRECURSOR TRANSMEMBRANE GLYCEROL-3-PHOSPHATE GPAT
MITOCHONDRION
Length = 194

Score = 458 (166.3 bits), Expect = 8.7e-43, P = 8.7e-43
Identities = 95/192 (49%), Positives = 126/192 (65%)

Query: 462 RRLIANLAEHILFTASKSCAIMSTHIVACLLLYHRHQIDLSTLVEFFVMKEEVLARDF 521
      R LI ++ EH++F S C+IMSTH+VACLLL R R G+ STL ED + E++LA
Sbjct: 3 RNLIRSIGEHVVFDSCMMCSIMSTHWACLLLTRWRNGVHRSTLEEDCDWLCEKILAEAG 62

Query: 522 DL-GFSGNS--EDVVMHAIQLLGNCVTTITHTSRNDFFITPSTTVPSVFEELNFYSNGVL 577
      D+ GFSG S +V +A +LLG+CVT+T RNDEF+I+P +VPS EL +YSN V+
Sbjct: 63 DIVGFGKSTKGSQIVKVACELLGSCVTVTDEDRNDEFYISPKNSVPSFIELAYYSNSVI 122

Query: 578 HVFINEAIIACSLYAVLNKRGLGGTSTPPNLIHQELVRKAASLCYLLSNEGTLISLPCQ 637
      F +++IIAC++Y++ NK GG NLISQELV A SLC L E PCQ
Sbjct: 123 CHFALKSIIACTIYSLNPKTKNGEAGGLGNLIHQELVEDALSCLDWLQYEFMFCRPCQ 182

Query: 638 TFYQVCHETVGK 649
      T ++CH T+GK
Sbjct: 183 TLRELCHNTLIGK 194

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Figure 4F

View Prodom PD042027

>PD042027 p2001.1 (6) PLSB(2) // ACYLTRANSFERASE GLYCEROL-3-PHOSPHATE MEMBRANE PHOSPHOLIPID GPAT BIOSYNTHESIS MUTANT

Length = 345

Score = 80 (33.2 bits), Expect = 0.11, Sum P(2) = 0.10
Identities = 31/129 (24%), Positives = 60/129 (46%)

Query: 465 IANLAEHILFTASKSCAIMSTHIVACLLYRHRQIGIDLSTLVE--DFFVMKEEVLARDFD 522

+ +LA+ I+ + + A+ ++ A LL ++ + L+E D ++ + D

Sbjct: 32 VNHLAKQIMTHINDAAAVNPMNLCATALISTRQALGEEQLIEQLDCYLKLLRNVPYSTD 91

Query: 523 LGFSGNS-EDVVMHAIQ--LLGNVCVTITHTSRNDEFFITPTTVPVSFEINFYNGVLHV 579

+ + E ++ HA Q LLG VT+ + D + V + +Y N VLH+

Sbjct: 92 ATLPDHTPERLIEHAEQNNLLG--VTVEKDTLGDILRLDRDNAVLI---MTYYRNNVLHL 145

Query: 580 FIMEALIIAC 588

F + A++AC

Sbjct: 146 FALPALVAC 154

Score = 62 (26.9 bits), Expect = 0.11, Sum P(2) = 0.10
Identities = 22/105 (20%), Positives = 48/105 (45%)

Query: 569 INFYNGVLHVTIMEAIIACSLYAVLNKRGISGPTSTPPNLIHQQLVKAASLCYLLSN 628

+ +Y N VLH+F + A++AC N+R IS++ L+R +L L

Sbjct: 135 MTYYRNNVLHLFALPALVACCFKN--NRR-----ISRDALIRFVRALYPFLQA 180

Query: 629 EGTISLPCQTFYQVCHETVGKFIQYIGILTVAEHDDQEDISPSLAE 673

E + + + +F++ G+L A + + + + + + +

Sbjct: 181 ELFLRWNEDELNDHIDQWINEFVRQGLLLSAGNQEDDTLTRNTSQ 225

Figure 4G

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View Prodom PD087501

>PD087501 p2001.1 (1) // AIP2-DLD1
    Length = 170

Score = 77 (32.2 bits), Expect = 5.1, P = 0.994
Identities = 31/114 (27%), Positives = 44/114 (38%)

Query:   51 WKES--LMSRKRPFGVGRCCYCTPQSWDKFFNPSPSLGLRNVIYINETHTRHGWLARR 108
          W ES L+ RK F RCC P K + L N +H W
Sbjct:   12 WNESEVLVDRKSKFQARCC---PLQNKDIPSLQELTQNNKSVSKASHMHMYAWRTAE 67

Query:   109 LSYVLFIQERDVHKGMEFATNVTENVLNSSR--VQ-EAIAEVAELNPDGSAQQ 158
          +S L +Q+ KG A + +N SR VQ + I + A+ G+ Q+
Sbjct:   68 VSNNLHLQQEQKKGNKANKSNNSHVNKSRNITVQPKNIEQGCADCGEAGAGQR 121
```

FIGURE 5A

	10	20	30	40	
1	MDESALT	LGTIDVSYLPHSS	EYSVGRCKHT	TSEEWGECGFR	56919.pro
1	MEESSVT	TVGTIDVSYLPSS	EYSLGRCKHT	TSEDWVDCGFK	MouseGPAT.PRO
1	MEESSVT	IGTIDVSYLPNS	EYSLGRCKHT	TNEDWVDCGFK	RatGPAT.PRO
	50	60	70	80	
41	PTVFRS	ATLKWKESLMSRKR	PFVGRCCYS	CTPQSWDKFFN	56919.pro
41	PTFFRS	ATLKWKESLMSRKR	PFVGRCCYS	CTPQSWERFFN	MouseGPAT.PRO
41	PTFFRS	ATLKWKESLMSRKR	PFVGRCCYS	CTPQSWERFFN	RatGPAT.PRO
	90	100	110	120	
81	PSIPSL	GLRNVIIYNETH	TRHRGWLARR	LSYVLFIQERDV	56919.pro
81	PSIPSL	GLRNVIIYNETH	TRHRGWLARR	LSYILFVQERDV	MouseGPAT.PRO
81	PSIPSL	GLRNVIIYNETH	TRHRGWLARR	LSYILFVQERDV	RatGPAT.PRO
	130	140	150	160	
121	HKG	MFATNVTENVLNS	SRVQEAAIAEVA	AAELNPDGSAQQQS	56919.pro
121	HKG	MFATSVTENVLNS	SRVQEAAIAEVA	AAELNPDGSAQQQS	MouseGPAT.PRO
121	HKG	MFATSTITDNVLNS	SRVQEAAIAEVA	AAELNPDGSAQQQS	RatGPAT.PRO
	170	180	190	200	
161	KAV	NKVKKKAKRILQ	EMVATVSPAMIR	L TGWVLLKLFNSF	56919.pro
161	KAI	QKVKRKARKILQ	EMVATVSPGMIR	L TGWVLLKLFNSF	MouseGPAT.PRO
161	KAI	QKVKRKARKILQ	EMVATVSPGMIR	L TGWVLLKLFNSF	RatGPAT.PRO
	210	220	230	240	
201	FWNI	QIHKGQLEMVKA	AATETNLP	LLF LFPVHRSHIDYLLLT	56919.pro
201	FWNI	QIHKGQLEMVKA	AATETNLP	LLF LFPVHRSHIDYLLLT	MouseGPAT.PRO
201	FWNI	QIHKGQLEMVKA	AATETNLP	LLF LFPVHRSHIDYLLLT	RatGPAT.PRO
	250	260	270	280	
241	FILF	CHNIKAPYIASG	NNLNIP	IFSTLIHKLGGFFIRRRRL	56919.pro
241	FILF	CHNIKAPYIASG	NNLNIP	VFSTLIHKLGGFFIRRRRL	MouseGPAT.PRO
241	FILF	CHNIKAPYIASG	NNLNIP	IFSTLIHKLGGFFIRRRRL	RatGPAT.PRO
	290	300	310	320	
281	DETP	DGRKDVLYRAL	LHGHIVE	LLRQQQFLEIFLEGTRSR	56919.pro
281	DETP	DGRKDILYRAL	LHGHIVE	LLRQQQFLEIFLEGTRSR	MouseGPAT.PRO
281	DETP	DGRKDILYRAL	LHGHIVE	LLRQQQFLEIFLEGTRSR	RatGPAT.PRO
	330	340	350	360	
321	SGKT	SCARAGLLSV	VVDTLSTNV	IPDILIIIPVGISYDRII	56919.pro
321	SGKT	SCARAGVLSV	VVNTLSSNT	IPDILVIPPVGISYDRII	MouseGPAT.PRO
321	SGKT	SCARAGLLSV	VVDTLSSNT	IPDILVIPPVGISYDRII	RatGPAT.PRO

FIGURE 5B

	370	380	390	400	
361	EGHYNGEQ	L GKPKKNE	SLWSVARGV	IRM LRKNY	G CVRVDF 56919.pro
361	EGHYNGEQ	L GKPKKNE	SLWSVARGV	IRM LRKNY	G YVRVDF MouseGPAT.PRO
361	EGHYNGEQ	L GKPKKNE	SLWSVARGV	IRM LRKNY	G YVRVDF RatGPAT.PRO
	410	420	430	440	
401	AQPFS	LKEYLES	QSQKPVSA	LLSLEQA	LLPAILPSRPSDA 56919.pro
401	AQPFS	LKEYLEG	QSQKPVSA	PLSLEQA	LLPAILPSRPN DV MouseGPAT.PRO
401	AQPFS	LKEYLEG	QSQKPVSA	PLSLEQA	LLPAILPSRPPDAA RatGPAT.PRO
	450	460	470	480	
441	ADEGR	DT SINES	RNATDES	LRRLIAN	LA EHILFTASKSC 56919.pro
441	ADEH	QDLSSNE	SRNPADE	A FRRLIAN	LA EHILFTASKSC MouseGPAT.PRO
441	AAEH	EDMSSNE	SRNAADE	A FRRLIAN	LA EHILFTASKSC RatGPAT.PRO
	490	500	510	520	
481	A	MSTHIV	ACLLLYR	HRHQGI	DLSTLVEDFFVMKEEV LARD 56919.pro
481	A	MSTHIV	ACLLLYR	HRHQGI	HLSTLVEDFFVMKEEV LARD MouseGPAT.PRO
481	A	MSTHIV	ACLLLYR	HRHQGI	HLSTLVEDFFVMKEEV LARD RatGPAT.PRO
	530	540	550	560	
521	F	DLGFSG	NSE	EDVVMHAI	QLLGNCVTITHTSRNDEFFITPS 56919.pro
521	F	DLGFSG	NSE	EDVVMHAI	QLLGNCVTITHTSRKDEFFITPS MouseGPAT.PRO
521	F	DLGFSG	NSE	EDVVMHAI	QLLGNCVTITHTSRKDEFFITPS RatGPAT.PRO
	570	580	590	600	
561	T	TVPSV	FELN	FYSNGV	LHV FIMEAIIACSLYAVLNKRGLG 56919.pro
561	T	TVPSV	FELN	FYSNGV	LHV FIMEAIIACSLYAVLNKRCSG MouseGPAT.PRO
561	T	TVPSV	FELN	FYSNGV	LHV FIMEAIIACSLYAVQNKRGSG RatGPAT.PRO
	610	620	630	640	
601	GPTST	TPPNLIS	QEQLV	RKAASLC	YLLSNEG TISLPCQTFY 56919.pro
601	GSAGG	LGNLIS	QEQLV	RKAASLC	YLLSNEG TISLPCQTFY MouseGPAT.PRO
601	GSAGG	LGNLIS	QEQLV	RKAASLC	YLLSNEG TISLPCQTFY RatGPAT.PRO
	650	660	670	680	
641	QVCH	ETV GKFI	QYGI	LTVAEH	DDQEDISP SLAEQQWDKKL 56919.pro
641	QVCH	ETV GKFI	QYGI	LTVAEH	DDQEDVSPGLAEQQWDKKL MouseGPAT.PRO
641	QVCQ	ETV GKFI	QYGI	LTVAEH	DDQEDVSPGLAEQQWNKKL RatGPAT.PRO
	690	700	710	720	
681	PEPL	SWRSDE	EEDEDS	DFGEEQ	RDCYLKVSQSKEHQQFITF 56919.pro
681	PE -	LNWRSDE	EEDEDS	DFGEEQ	RDCYLKVSQSKEHQQFITF MouseGPAT.PRO
681	PEPL	LNWRSDE	EEDEDS	DFGEEQ	RDCYLKVSQAKEHQQFITF RatGPAT.PRO

	730	740	750	760	
721	L Q R L L G P L L E A Y S S A A I F V H N F S G P V P E P E Y L Q K L H K Y L I				56919.pro
720	L Q R L L G P L L E A Y S S A A I F V H N F S G P V P E S E Y L Q K L H R Y L I				MouseGPAT.PRO
721	L Q R L L G P L L E A Y S S A A I F V H T F R G P V P E S E Y L Q K L H R Y L L				RatGPAT.PRO
	770	780	790	800	
761	T R T E R N V A V Y A E S A T Y C L V K N A V K M F K D I G V F K E T K Q K R V				56919.pro
760	T R T E R N V A V Y A E S A T Y C L V K N A V K M F K D I G V F K E T K Q K R V				MouseGPAT.PRO
761	T R T E R N V A V Y A E S A T Y C L V K N A V K M F K D I G V F K E T K Q K R A				RatGPAT.PRO
	810	820			
801	S V L E L S S T F L P Q C N R Q K L L E Y I L S F V V L				56919.pro
800	S V L E L S S T F L P Q C N R Q K L L E Y I L S F V V L				MouseGPAT.PRO
801	S V L E L S T T F L P Q G S R Q K L L E Y I L S F V V L				RatGPAT.PRO

[illegible]

Acyltransferase catalytic motif-I

I F L E G T R S R	56919.pro
I F L E G T R S R	MouseGPAT.PRO
I F L E G T R S R	RatGPAT.PRO
Y F V E G G R S R	EcoliGPAT.PRO

Acyltransferase catalytic motif-II

H R S H I D	56919.pro
H R S H I D	MouseGPAT.PRO
H R S H I D	RatGPAT.PRO
H R S H M D	EcoliGPAT.PRO

Acyltransferase catalytic motif-III

I L I I P V	56919.pro
I L V I P V	MouseGPAT.PRO
I L V I P V	RatGPAT.PRO
I T L I P I	EcoliGPAT.PRO

Acyltransferase signature motif

G G F F I R R	56919.pro
G G F F I R R	MouseGPAT.PRO
G G F F I R R	RatGPAT.PRO
G A F F I R R	EcoliGPAT.PRO

FIGURE 6

Figure 7

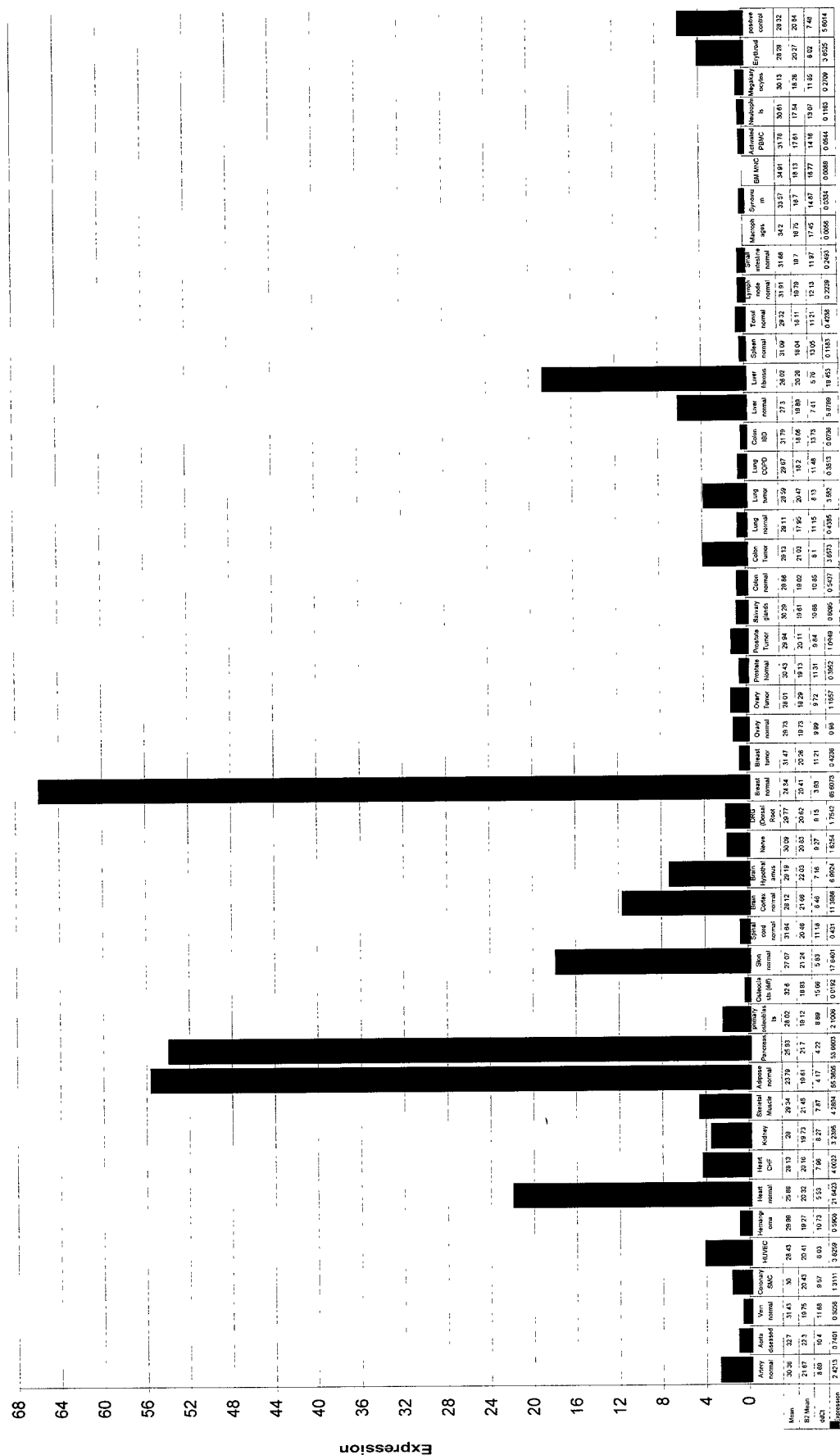


FIGURE 8

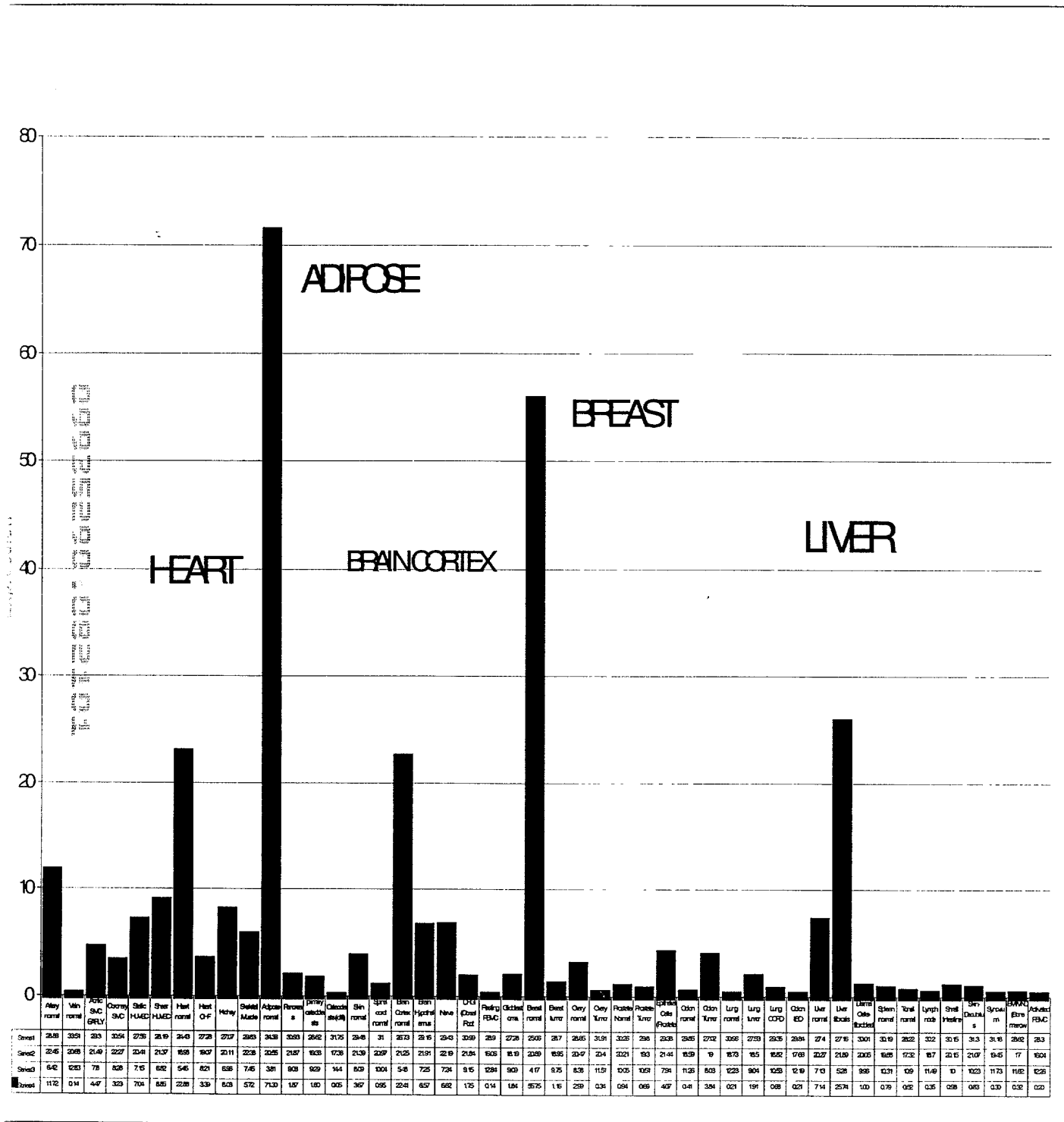


FIGURE 9

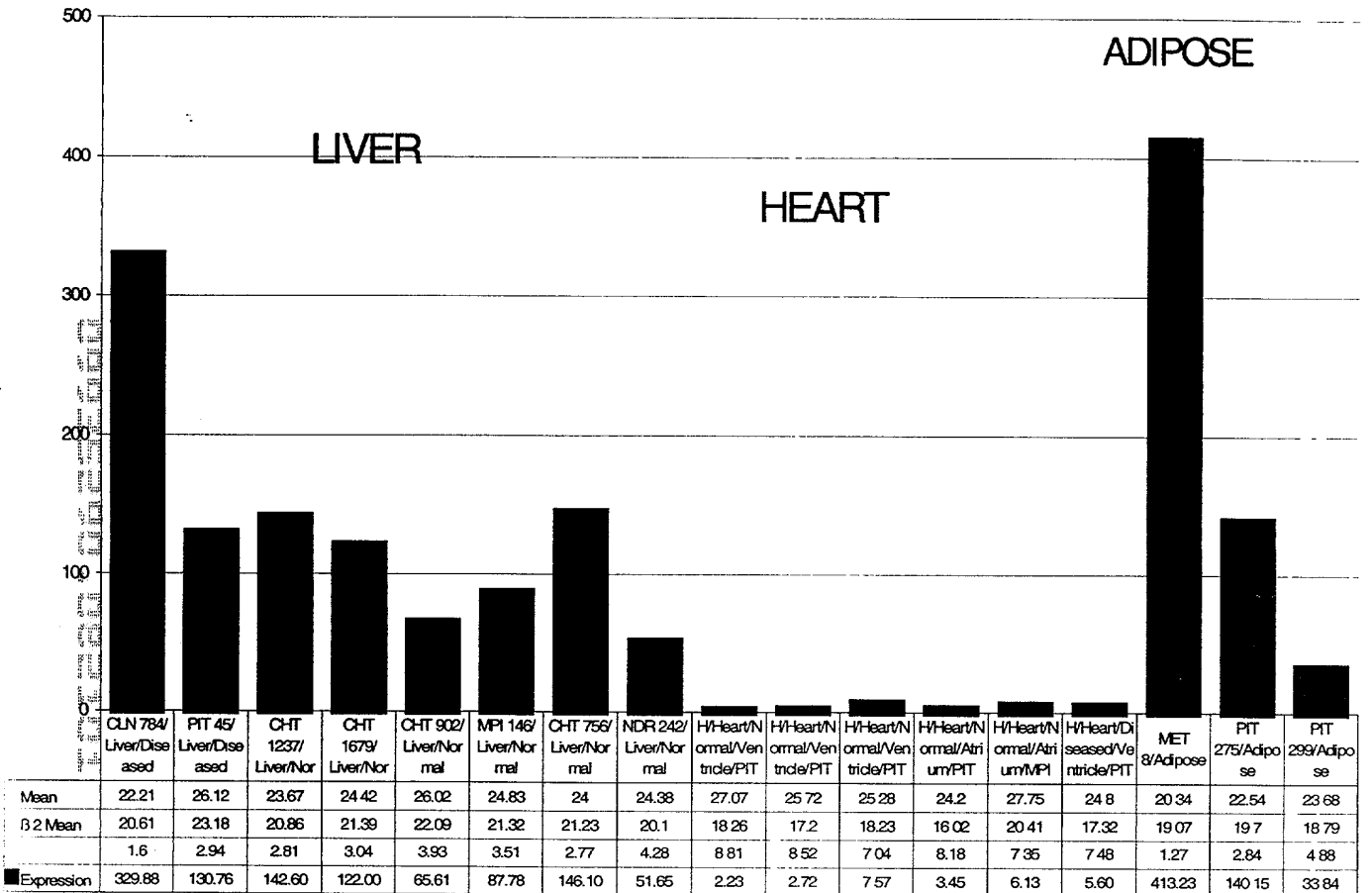


FIGURE 10A

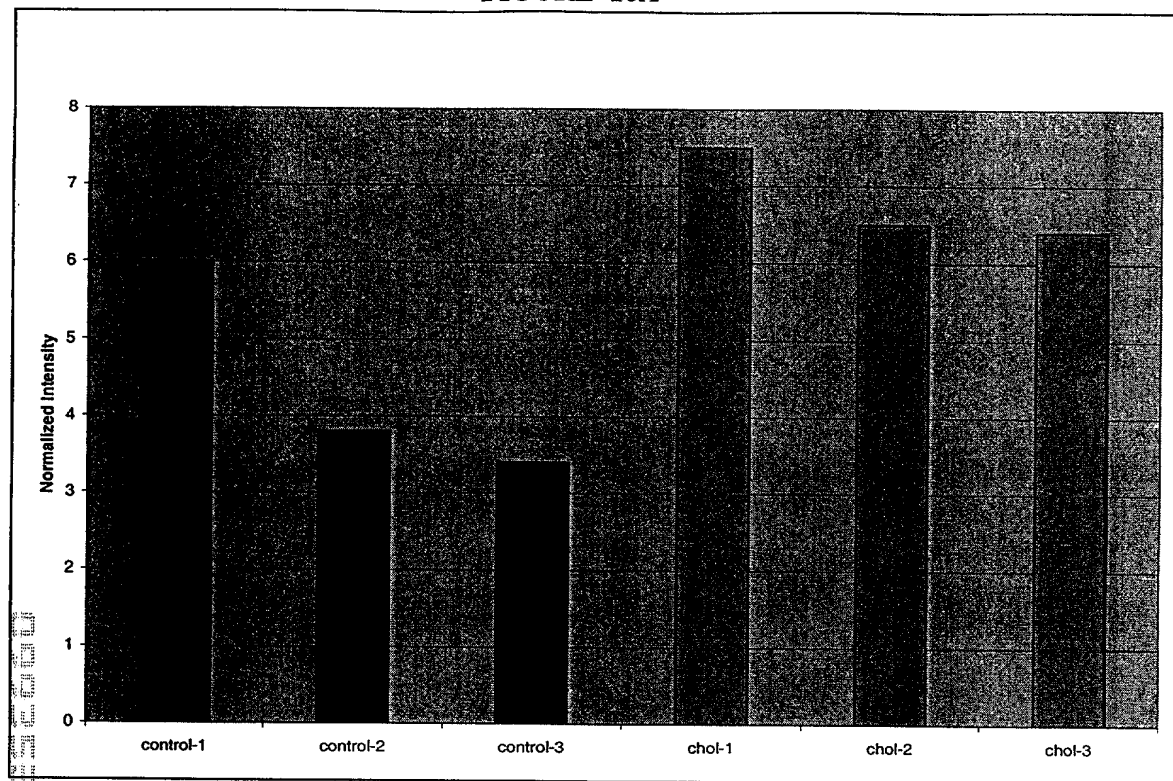


FIGURE 10B

